



IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/825,127

DATE: 08/04/2004
TIME: 08:30:13

Input Set : N:\Crf3\RULE60\10825127.raw
Output Set: N:\CRF4\08042004\J825127.raw

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1 <110> APPLICANT: FUKUCHI, Naoyuki
2     FUTAKI, Fumie
3     KITO, Morikazu
4     SATO, Seiichi
5     KAJIURA, Takayuki
6     ONO, Yukitsugu
7     TANAKA,, Akiko
8     SHINOZAKI, Junko
9 <120> TITLE OF INVENTION: Substance with Antithrombic Activity and Method for
10 Detecting
11 Glycocalicin
12 <130> FILE REFERENCE: 198804US0PCT
13 <140> CURRENT APPLICATION NUMBER: US/10/825,127
14 <141> CURRENT FILING DATE: 2004-04-16
15 <150> PRIOR APPLICATION NUMBER: US/09/673,245
16 <151> PRIOR FILING DATE: 2000-10-23
17 <150> PRIOR APPLICATION NUMBER: PCT/JP99/00089
18 <151> PRIOR FILING DATE: 1998-01-13
19 <150> PRIOR APPLICATION NUMBER: JP 10-113962
20 <151> PRIOR FILING DATE: 1998-04-23
21 <160> NUMBER OF SEQ ID NOS: 14
22 <170> SOFTWARE: PatentIn version 3.1
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27 <213> ORGANISM: ARTIFICIAL SEQUENCE
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29 <223> OTHER INFORMATION: SYNTHETIC DNA
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36 <213> ORGANISM: ARTIFICIAL SEQUENCE
37 <220> FEATURE:
38 <223> OTHER INFORMATION: SYNTHETIC DNA
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44 <212> TYPE: DNA
45 <213> ORGANISM: ARTIFICIAL SEQUENCE
46 <220> FEATURE:

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ENTERED

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47 <223> OTHER INFORMATION: SYNTHETIC DNA
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 62 1 5 10 15
 63 gta tca tct gtc ttc atc ttc ccc cca aag ccc aag gat gtg ctc acc 96
 64 Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr
 65 20 25 30
 66 att act ctg act cct aag gtc acg tgt gtt gtg gta gac atc agc aag 144
 67 Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys
 68 35 40 45
 69 gat gat ccc gag gtc cag ttc acg tgg ttt gta gat gat gtg gag gtg 192
 70 Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val
 71 50 55 60
 72 cac aca gct cag acg caa ccc cgg gag gag cag ttc aac agc act ttc 240
 73 His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
 74 65 70 75 80
 75 cgc tca gtc agt gaa ctt ccc atc atg cac cag gac tgg ctc aat ggc 288
 76 Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly
 77 85 90 95
 78 aag gag ttc aaa tgc agg gta aac agt gca gct ttc cct gcc ccc atc 336
 79 Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile
 80 100 105 110
 81 gag aaa acc atc tcc aaa acc aaa ggc aga ccg aag gct cca cag gtg 384
 82 Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val
 83 115 120 125
 84 tac acc att cca cct ccc aag gag cag atg gcc aag gat aaa gtc agt 432
 85 Tyr Thr Ile Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser
 86 130 135 140
 87 ctg acc tgc atg ata aca gac ttc ttc cct gaa gac att act gtg gag 480
 88 Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu
 89 145 150 155 160
 90 tgg cag tgg aat ggg cag cca gcg gag aac tac aag aac act cag ccc 528
 91 Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro
 92 165 170 175
 93 atc atg gac aca gat ggc tct tac ttc gtc tac agc aag ctc aat gtg 576
 94 Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val
 95 180 185 190
 96 cag aag agc aac tgg gag gca gga aat act ttc acc tgc tct gtg tta 624

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97 Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu
 98 195 200 205
 99 cat gag ggc ctg cac aac cac cat act gag aag agc ctc tcc cac tct 672
 100 His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser
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 103 Pro Gly Lys
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 107 <211> LENGTH: 227
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 109 <213> ORGANISM: Mus musculus
 110 <400> SEQUENCE: 5
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 114 20 25 30
 115 Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys 45
 116 35 40 45
 117 Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val 60
 118 50 55 60
 119 His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe 80
 120 65 70 75 80
 121 Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly 95
 122 85 90 95
 123 Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile 110
 124 100 105 110
 125 Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val 125
 126 115 120 125
 127 Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser 140
 128 130 135 140
 129 Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu 160
 130 145 150 155 160
 131 Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro 175
 132 165 170 175
 133 Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val 190
 134 180 185 190
 135 Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu 205
 136 195 200 205
 137 His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser
 138 210 215 220
 139 Pro Gly Lys
 140 225
 142 <210> SEQ ID NO: 6
 143 <211> LENGTH: 1689
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 145 <213> ORGANISM: ARTIFICIAL SEQUENCE
 146 <220> FEATURE:
 147 <223> OTHER INFORMATION: SYNTHETIC DNA

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149 <222> LOCATION: (1)..(1686)
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152 <222> LOCATION: (1)..(48)
153 <223> OTHER INFORMATION:
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155 <222> LOCATION: (49)..()
156 <223> OTHER INFORMATION:
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160 -15 -10 -5 -1
161 cac ccc atc tgt gag gtc tcc aaa gtg gcc agc cac cta gaa gtg aac 96
162 His Pro Ile Cys Glu Val Ser Lys Val Ala Ser His Leu Glu Val Asn
163 1 5 10 15
164 tgt gac aag agg aat ctg aca gcg ctg cct cca gac ctg ccg aaa gac 144
165 Cys Asp Lys Arg Asn Leu Thr Ala Leu Pro Pro Asp Leu Pro Lys Asp
166 20 25 30
167 aca acc atc ctc cac ctg agt gag aac ctc ctg tac acc ttc tcc ctg 192
168 Thr Thr Ile Leu His Leu Ser Glu Asn Leu Leu Tyr Thr Phe Ser Leu
169 35 40 45
170 gca acc ctg atg cct tac act cgc ctc act cag ctg aac cta gat agg 240
171 Ala Thr Leu Met Pro Tyr Thr Arg Leu Thr Gln Leu Asn Leu Asp Arg
172 50 55 60
173 tgc gag ctc acc aag ctc cag gtc gat ggg acg ctg cca gtg ctg ggg 288
174 Cys Glu Leu Thr Lys Leu Gln Val Asp Gly Thr Leu Pro Val Leu Gly
175 65 70 75 80
176 acc ctg gat cta tcc cac aat cag ctg caa agc ctg ccc ttg cta ggg 336
177 Thr Leu Asp Leu Ser His Asn Gln Leu Gln Ser Leu Pro Leu Leu Gly
178 85 90 95
179 cag aca ctg cct gct ctc acc gtc ctg gac gtc tcc ttc aac cgg ctg 384
180 Gln Thr Leu Pro Ala Leu Thr Val Leu Asp Val Ser Phe Asn Arg Leu
181 100 105 110
182 acc tcg ctg cct ctt ggt gcc ctg cgt ggt ctt ggc gaa ctc caa gag 432
183 Thr Ser Leu Pro Leu Gly Ala Leu Arg Gly Leu Gly Glu Leu Gln Glu
184 115 120 125
185 ctc tac ctg aaa ggc aat gag ctg aag acc ctg ccc cca ggg ctc ctg 480
186 Leu Tyr Leu Lys Gly Asn Glu Leu Lys Thr Leu Pro Pro Gly Leu Leu
187 130 135 140
188 acg ccc aca ccc aag ctg gag aag ctc agt ctg gct aac aac aac ttg 528
189 Thr Pro Thr Pro Lys Leu Glu Lys Leu Ser Leu Ala Asn Asn Asn Leu
190 145 150 155 160
191 act gag ctc ccc gct ggg ctc ctg aat ggg ctg gag aat ctc gac acc 576
192 Thr Glu Leu Pro Ala Gly Leu Leu Asn Gly Leu Glu Asn Leu Asp Thr
193 165 170 175
194 ctt ctc ctc caa gag aac tcg ctg tat aca ata cca aag ggc ttt ttt 624
195 Leu Leu Leu Gln Glu Asn Ser Leu Tyr Thr Ile Pro Lys Gly Phe Phe
196 180 185 190

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197	ggg tcc cac ctc ctg cct ttt gct ttt ctc cac ggg aac ccc tgg tta	672
198	Gly Ser His Leu Leu Pro Phe Ala Phe Leu His Gly Asn Pro Trp Leu	
199	195 200 205	
200	tgc aac tgt gag atc ctc tat ttt cgt cgc tgg ctg cag gac aat gct	720
201	Cys Asn Cys Glu Ile Leu Tyr Phe Arg Arg Trp Leu Gln Asp Asn Ala	
202	210 215 220	
203	gaa aat gtc tac gta tgg aag caa ggt gtg gac gtc aag gcc atg acc	768
204	Glu Asn Val Tyr Val Trp Lys Gln Gly Val Asp Val Lys Ala Met Thr	
205	225 230 235 240	
206	tct aac gtg gcc agt gtg cag tgt gac aat tca gac aag ttt ccc gtc	816
207	Ser Asn Val Ala Ser Val Gln Cys Asp Asn Ser Asp Lys Phe Pro Val	
208	245 250 255	
209	tac aaa tac cca gga aag ggg tgc ccc acc ctt ggt gat gaa ggt gac	864
210	Tyr Lys Tyr Pro Gly Lys Gly Cys Pro Thr Leu Gly Asp Glu Gly Asp	
211	260 265 270	
212	aca gac cta tat gat tac tac cca gaa gag gac act gag ggc gat aag	912
213	Thr Asp Leu Tyr Asp Tyr Pro Glu Glu Asp Thr Gly Asp Lys	
214	275 280 285	
215	gtg cgt gcc aca agg act gtg gtc aag ttc ccc acc aaa gcc cat aca	960
216	Val Arg Ala Thr Arg Thr Val Val Lys Phe Pro Thr Lys Ala His Thr	
217	290 295 300	
218	acc ccc tgg ggt cta ttc tac tca tgg tcc act gct tct cta gac gtg	1008
219	Thr Pro Trp Gly Leu Phe Tyr Ser Trp Ser Thr Ala Ser Leu Asp Val	
220	305 310 315 320	
221	ccc agg gat tgt ggt aag cct tgc ata tgt aca gtc cca gaa gta	1056
222	Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val	
223	325 330 335	
224	tca tct gtc ttc atc ttc ccc cca aag ccc aag gat gtg ctc acc att	1104
225	Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile	
226	340 345 350	
227	act ctg act cct aag gtc acg tgt gtt gtg gta gac atc agc aag gat	1152
228	Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp	
229	355 360 365	
230	gat ccc gag gtc cag ttc agc tgg ttt gta gat gat gtg gag gtg cac	1200
231	Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His	
232	370 375 380	
233	aca gct cag acg caa ccc cgg gag gag cag ttc aac agc act ttc cgc	1248
234	Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg	
235	385 390 395 400	
236	tca gtc agt gaa ctt ccc atc atg cac cag gac tgg ctc aat ggc aag	1296
237	Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys	
238	405 410 415	
239	gag ttc aaa tgc agg gta aac agt gca gct ttc cct gcc ccc atc gag	1344
240	Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu	
241	420 425 430	
242	aaa acc atc tcc aaa acc aaa ggc aga ccg aag gct cca cag gtg tac	1392
243	Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr	
244	435 440 445	
245	acc att cca cct ccc aag gag cag atg gcc aag gat aaa gtc agt ctg	1440

VERIFICATION SUMMARY

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Output Set: N:\CRF4\08042004\J825127.raw

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